

RAW SEQUENCE LISTING

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Application Serial Number: 10/771,833
Source: EFW0
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/771,833

DATE: 10/29/2004

TIME: 11:12:12

Input Set : A:\39363106.app

Output Set: N:\CRF4\10292004\J771833.raw

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3 <110> APPLICANT: MILBURN, MICHAEL V.
5 <120> TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
7 <130> FILE REFERENCE: 039363-1106
9 <140> CURRENT APPLICATION NUMBER: 10/771,833
10 <141> CURRENT FILING DATE: 2004-02-03
12 <150> PRIOR APPLICATION NUMBER: 60/485,627
13 <151> PRIOR FILING DATE: 2003-07-07
15 <150> PRIOR APPLICATION NUMBER: 60/444,734
16 <151> PRIOR FILING DATE: 2003-02-03
18 <160> NUMBER OF SEQ ID NOS: 31
20 <170> SOFTWARE: PatentIn Ver. 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 875
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
28 Met Glu Arg Ala Gly Pro Ser Phe Gly Gln Gln Arg Gln Gln Gln Gln
29   1           5           10           15
31 Pro Gln Gln Gln Lys Gln Gln Gln Arg Asp Gln Asp Ser Val Glu Ala
32           20           25           30
34 Trp Leu Asp Asp His Trp Asp Phe Thr Phe Ser Tyr Phe Val Arg Lys
35           35           40           45
37 Ala Thr Arg Glu Met Val Asn Ala Trp Phe Ala Glu Arg Val His Thr
38           50           55           60
40 Ile Pro Val Cys Lys Glu Gly Ile Arg Gly His Thr Glu Ser Cys Ser
41   65           70           75           80
43 Cys Pro Leu Gln Gln Ser Pro Arg Ala Asp Asn Ser Val Pro Gly Thr
44           85           90           95
46 Pro Thr Arg Lys Ile Ser Ala Ser Glu Phe Asp Arg Pro Leu Arg Pro
47           100          105          110
49 Ile Val Val Lys Asp Ser Glu Gly Thr Val Ser Phe Leu Ser Asp Ser
50           115          120          125
52 Glu Lys Lys Glu Gln Met Pro Leu Thr Pro Pro Arg Phe Asp His Asp
53           130          135          140
55 Glu Gly Asp Gln Cys Ser Arg Leu Leu Glu Leu Val Lys Asp Ile Ser
56 145           150           155           160
58 Ser His Leu Asp Val Thr Ala Leu Cys His Lys Ile Phe Leu His Ile
59           165           170           175
61 His Gly Leu Ile Ser Ala Asp Arg Tyr Ser Leu Phe Leu Val Cys Glu
62           180           185           190
64 Asp Ser Ser Asn Asp Lys Phe Leu Ile Ser Arg Leu Phe Asp Val Ala
65           195           200           205
67 Glu Gly Ser Thr Leu Glu Glu Val Ser Asn Asn Cys Ile Arg Leu Glu

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68      210      215      220
70 Trp Asn Lys Gly Ile Val Gly His Val Ala Ala Leu Gly Glu Pro Leu
71 225      230      235      240
73 Asn Ile Lys Asp Ala Tyr Glu Asp Pro Arg Phe Asn Ala Glu Val Asp
74      245      250      255
76 Gln Ile Thr Gly Tyr Lys Thr Gln Ser Ile Leu Cys Met Pro Ile Lys
77      260      265      270
79 Asn His Arg Glu Glu Val Val Gly Val Ala Gln Ala Ile Asn Lys Lys
80      275      280      285
82 Ser Gly Asn Gly Gly Thr Phe Thr Glu Lys Asp Glu Lys Asp Phe Ala
83      290      295      300
85 Ala Tyr Leu Ala Phe Cys Gly Ile Val Leu His Asn Ala Gln Leu Tyr
86 305      310      315      320
88 Glu Thr Ser Leu Leu Glu Asn Lys Arg Asn Gln Val Leu Leu Asp Leu
89      325      330      335
91 Ala Ser Leu Ile Phe Glu Glu Gln Gln Ser Leu Glu Val Ile Leu Lys
92      340      345      350
94 Lys Ile Ala Ala Thr Ile Ile Ser Phe Met Gln Val Gln Lys Cys Thr
95      355      360      365
97 Ile Phe Ile Val Asp Glu Asp Cys Ser Asp Ser Phe Ser Ser Val Phe
98      370      375      380
100 His Met Glu Cys Glu Glu Leu Glu Lys Ser Ser Asp Thr Leu Thr Arg
101 385      390      395      400
103 Glu His Asp Ala Asn Lys Ile Asn Tyr Met Tyr Ala Gln Tyr Val Lys
104      405      410      415
106 Asn Thr Met Glu Pro Leu Asn Ile Pro Asp Val Ser Lys Asp Lys Arg
107      420      425      430
109 Phe Pro Trp Thr Thr Glu Asn Thr Gly Asn Val Asn Gln Gln Cys Ile
110      435      440      445
112 Arg Ser Leu Leu Cys Thr Pro Ile Lys Asn Gly Lys Lys Asn Lys Val
113      450      455      460
115 Ile Gly Val Cys Gln Leu Val Asn Lys Met Glu Glu Asn Thr Gly Lys
116 465      470      475      480
118 Val Lys Pro Phe Asn Arg Asn Asp Glu Gln Phe Leu Glu Ala Phe Val
119      485      490      495
121 Ile Phe Cys Gly Leu Gly Ile Gln Asn Thr Gln Met Tyr Glu Ala Val
122      500      505      510
124 Glu Arg Ala Met Ala Lys Gln Met Val Thr Leu Glu Val Leu Ser Tyr
125      515      520      525
127 His Ala Ser Ala Ala Glu Glu Glu Thr Arg Glu Leu Gln Ser Leu Ala
128      530      535      540
130 Ala Ala Val Val Pro Ser Ala Gln Thr Leu Lys Ile Thr Asp Phe Ser
131 545      550      555      560
133 Phe Ser Asp Phe Glu Leu Ser Asp Leu Glu Thr Ala Leu Cys Thr Ile
134      565      570      575
136 Arg Met Phe Thr Asp Leu Asn Leu Val Gln Asn Phe Gln Met Lys His
137      580      585      590
139 Glu Val Leu Cys Arg Trp Ile Leu Ser Val Lys Lys Asn Tyr Arg Lys
140      595      600      605

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142 Asn Val Ala Tyr His Asn Trp Arg His Ala Phe Asn Thr Ala Gln Cys
143      610                      615                      620
145 Met Phe Ala Ala Leu Lys Ala Gly Lys Ile Gln Asn Lys Leu Thr Asp
146 625                      630                      635                      640
148 Leu Glu Ile Leu Ala Leu Leu Ile Ala Ala Leu Ser His Asp Leu Asp
149      645                      650                      655
151 His Arg Gly Val Asn Asn Ser Tyr Ile Gln Arg Ser Glu His Pro Leu
152      660                      665                      670
154 Ala Gln Leu Tyr Cys His Ser Ile Met Glu His His His Phe Asp Gln
155      675                      680                      685
157 Cys Leu Met Ile Leu Asn Ser Pro Gly Asn Gln Ile Leu Ser Gly Leu
158      690                      695                      700
160 Ser Ile Glu Glu Tyr Lys Thr Thr Leu Lys Ile Ile Lys Gln Ala Ile
161 705                      710                      715                      720
163 Leu Ala Thr Asp Leu Ala Leu Tyr Ile Lys Arg Arg Gly Glu Phe Phe
164      725                      730                      735
166 Glu Leu Ile Arg Lys Asn Gln Phe Asn Leu Glu Asp Pro His Gln Lys
167      740                      745                      750
169 Glu Leu Phe Leu Ala Met Leu Met Thr Ala Cys Asp Leu Ser Ala Ile
170      755                      760                      765
172 Thr Lys Pro Trp Pro Ile Gln Gln Arg Ile Ala Glu Leu Val Ala Thr
173      770                      775                      780
175 Glu Phe Phe Asp Gln Gly Asp Arg Glu Arg Lys Glu Leu Asn Ile Glu
176 785                      790                      795                      800
178 Pro Thr Asp Leu Met Asn Arg Glu Lys Lys Asn Lys Ile Pro Ser Met
179      805                      810                      815
181 Gln Val Gly Phe Ile Asp Ala Ile Cys Leu Gln Leu Tyr Glu Ala Leu
182      820                      825                      830
184 Thr His Val Ser Glu Asp Cys Phe Pro Leu Leu Asp Gly Cys Arg Lys
185      835                      840                      845
187 Asn Arg Gln Lys Trp Gln Ala Leu Ala Glu Gln Gln Glu Lys Met Leu
188      850                      855                      860
190 Ile Asn Gly Glu Ser Gly Gln Ala Lys Arg Asn
191 865                      870                      875
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 3106
196 <212> TYPE: DNA
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 2
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201 gggctctcgag gccgagtcct gttctttctga gggacggacc ccagctgggg tggaaaagca 120
202 gtaccagaga gcctccgagg cgcgcggtgc caaccatgga gcgggccggc cccagcttcg 180
203 ggcagcagcg acagcagcag cagccccagc agcagaagca gcagcagagg gatcaggact 240
204 cggtcgaagc atggctggac gatcactggg actttacctt ctcatacttt gttagaaaag 300
205 ccaccagaga aatggtcaat gcattggtttg ctgagagagt tcacaccatc cctgtgtgca 360
206 aggaaggtat cagaggccac accgaatctt gctcttgtcc cttgcagcag agtcctcgtg 420
207 cagataacag tgtccctgga acaccaacca ggaaaatctc tgccctctgaa tttgaccggc 480
208 ctcttagacc cattgttgtc aaggattctg aggggaactgt gagcttcctc tctgactcag 540
209 aaaagaagga acagatgcct ctaacccctc caagggttga tcatgatgaa ggggaccagt 600

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210 gctcaagact cttggaatta gtgaaggata tttctagtca tttggatgtc acagccttat 660
211 gtcacaaaat tttcttgcac atccatggac tgatatctgc tgaccgctat tccctgttcc 720
212 ttgtctgtga agacagctcc aatgacaagt ttcttatcag ccgcctcttt gatgttgctg 780
213 aaggttcaac actggaagaa gtttcaaata actgtatccg cttagaatgg aacaaaggca 840
214 ttgtgggaca tgtggcagcg cttggtgagc ccttgaacat caaagatgca tatgaggatc 900
215 ctcggttcaa tgcagaagtt gaccaaatta caggctacaa gacacaaagc attctttgta 960
216 tgccaattaa gaatcatagg gaagagggtt ttggtgtagc ccaggccatc aacaagaaat 1020
217 caggaaacgg tgggacattt actgaaaaag atgaaaagga ctttgctgct tatttggcat 1080
218 tttgtggtat tgttcttcat aatgctcagc tctatgagac ttcactgctg gagaacaaga 1140
219 gaaatcaggt gctgcttgac cttgctagtt taatttttga agaacaacaa tcattagaag 1200
220 taattttgaa gaaaatagct gccactatta tctctttcat gcaagtgcag aaatgcacca 1260
221 ttttcatagt ggatgaagat tgctccgatt ctttttctag tgtgtttcac atggagtgtg 1320
222 aggaattaga aaaatcatct gatacattaa caagggaaca tgatgcaaac aaaatcaatt 1380
223 acatgtatgc tcagtatgtc aaaaatacta tgggaacct taatatccca gatgtcagta 1440
224 aggataaaag atttccctgg acaactgaaa atacaggaaa tgtaaaccag cagtgcatta 1500
225 gaagtttgct ttgtacacct ataaaaaatg gaaagaagaa taaagttata ggggtttgcc 1560
226 aacttgttaa taagatggag gagaatactg gcaagggttaa gcctttcaac cgaaatgacg 1620
227 aacagtttct ggaagctttt gtcactttt gtggcttggg gatccagaac acgcagatgt 1680
228 atgaagcagt ggagagagcc atggccaagc aaatggtcac attggaggtt ctgtcgtatc 1740
229 atgcttcagc agcagaggaa gaaacaagag agctacagtc gttagcggct gctgtggtgc 1800
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231 tggaaacagc actgtgtaca attcggatgt ttactgacct caaccttggt cagaacttcc 1920
232 agatgaaaca tgaggttctt tgcagatgga ttttaagtgt taagaagaat tatcggaaga 1980
233 atgttgctta tcataattgg agacatgcct ttaatacagc tcagtgcagc tttgctgtc 2040
234 taaaagcagg caaaattcag aacaagctga ctgacctgga gatacttgca ttgctgattg 2100
235 ctgactaag ccacgatttg gatcacctg gtgtgaataa ctcttacata cagcgaagtg 2160
236 aacatccact tgcccagctt tactgccatt caatcatgga acaccatcat tttgaccagt 2220
237 gcctgatgat tcttaatagt ccaggcaatc agattctcag tggcctctcc attgaagaat 2280
238 ataagaccac gttgaaaata atcaagcaag ctatttttagc tacagaccta gcactgtaca 2340
239 ttaagaggcg aggagaattt tttgaactta taagaaaaaa tcaattcaat ttggaagatc 2400
240 ctcatcaaaa ggagttgttt ttggcaatgc tgatgacagc ttgtgatctt tctgcaatta 2460
241 caaaaccttg gctatttcaa caacggatag cagaacttgt agcaactgaa ttttttgatc 2520
242 aaggagacag agagagaaaa gaactcaaca tagaaccac tgatctaatt aacagggaga 2580
243 agaaaaacaa aatcccaagt atgcaagttg ggttcataga tgccatctgc ttgcaactgt 2640
244 atgaggccct gaccacgtg tcagaggact gtttcccttt gctagatggc tgcagaaaga 2700
245 acaggcagaa atggcaggcc cttgcagaac agcaggagaa gatgctgatt aatggggaaa 2760
246 gcggccaggc caagcggaac tgagtggcct atttcatgca gagttgaagt ttacagagat 2820
247 ggtgtgttct gcaatatgcc tagtttctta cacactgtct gtatagtgtc tgtatttggg 2880
248 atatactttg ccactgctgt attttttatt ttgcacaact tttgagagta tagcatgaat 2940
249 gtttttagag gactattaca tttttttgt atatttgggt tatgctactg aactgaaagg 3000
250 atcaacaaca tccactgtta gcacattgat aaaagcattg tttgtgatat ttogtgtact 3060
251 gcaaagtgtg tgcagtattc ttgcactgag gtttttttgc ttggggg 3106

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254 <210> SEQ ID NO: 3

255 <211> LENGTH: 33

256 <212> TYPE: DNA

257 <213> ORGANISM: Artificial Sequence

259 <220> FEATURE:

260 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

262 <400> SEQUENCE: 3

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263 gtcgtatcat atgtcagcag cagaggaaga aac 33
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 32
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
274 <400> SEQUENCE: 4
275 tctgcagtcg acaggccact cagttccgct tg 32
278 <210> SEQ ID NO: 5
279 <211> LENGTH: 391
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Pet15S construct
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (108)..(170)
290 <400> SEQUENCE: 5
291 agatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 60
293 ttcccctcta gaaataattt tgtttaactt taagaaggag atatacc atg ggc agc 116
294 Met Gly Ser
295 1
297 agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
298 Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
299 5 10 15
301 cat atg ggatccgaa ttcaaaggcc tacgtcgact agagcctgca gtctcgacca 220
302 His Met
303 20
305 tcatcatcat catcattaat aaaagggcga attccagcac actggcggcc gttactagt 280
307 gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa 340
309 taactagcat aacccttgg ggctctataa cgggtcttga ggggtttttt g 391
312 <210> SEQ ID NO: 6
313 <211> LENGTH: 21
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: Pet15S construct
320 <400> SEQUENCE: 6
321 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
322 1 5 10 15
324 Arg Gly Ser His Met
325 20
329 <210> SEQ ID NO: 7
330 <211> LENGTH: 6
331 <212> TYPE: PRT
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Description of Artificial Sequence: 6-His tag

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